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Docket No. 2786-0199P

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40. (New) A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient the expression vector of Claim 33.

41. (New) A pharmaceutical composition comprising a pharmaceutically acceptable carrier as an active ingredient the purified antibody of Claim 31.

42. (New) A pharmaceutical composition for treatment of diseases which can be ameliorated, cured or prevented by reducing the level of at least one of the CD40R variants of Claim 26.

43. (New) A method for detecting the presence of at least one variant nucleic acid sequence of CD40R in a biological sample, comprising the steps of:

(a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 26, and

(b) detecting said hybridization complex;

wherein the presence of said hybridization complex correlates with the presence of at least one variant nucleic acid sequence in the said biological sample.

44. (New) A method for determining the level of variant nucleic acid sequences of CD40R in a biological sample comprising the steps of:


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- (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 26; and
- (b) determining the amount of hybridization complexes and normalizing said amount to provide the level of the at least one variant nucleic acid sequences in the sample.

45. (New) A method for determining the ratio between the level of the nucleic acid sequence of a CD40R variant in a first biological sample and the level of the original CD40R sequence from which the variant has been varied by alternative splicing, in a second biological sample comprising:

- (a) determining the level of the CD40R variant nucleic acid sequence in the first biological sample according to the method of Claim 44,
- (b) determining the level of the CD40R original sequence in the second biological sample; and
- (c) comparing the levels obtained in (a) and (b) to give said ratio.

46. (New) A method according to Claim 45, wherein said first and said second biological samples are the same sample.

47. (New) A method according to Claim 45, wherein the nucleic acid material of said biological sample are mRNA transcripts.

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48. (New) A method according to Claim 46, where the nucleic acid sequence is present in a nucleic acid chip.

49. (New) A method for identifying candidate compounds capable of binding to the amino acid sequence of Claim 28 and affecting the binding affinity of said sequences to at least one ligand of CD40, the method comprising:

- (i) providing any one of the amino acid sequences as defined in Claim 28;
- (ii) contacting a candidate compound with said amino acid sequence in the presence of at least one ligand of CD40;
- (iii) determining the effect of said candidate compound on the binding of said amino acid to said ligand and selecting those compounds which show a significant effect on said binding.

50. (New) A method for detecting any one of the amino acid sequences of Claim 28 in a biological sample, comprising:

- (a) contacting with said biological sample an antibody which binds specifically to an amino acid sequence present in any of the amino acid sequence of Claim 28 and not present in native CD40R, thereby forming any antibody-antigen complex; and